

87(5):1806-1810); the human IL-9 receptor (approximately 29.7% identity over a 158 amino acid overlap; SEQ ID NO:7; SP Accession Number Q01113; Renauld *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89(12):5690-5694; Chang *et al.* (1994) *Blood* 83(11):3199-3205; Kermouni *et al.* (1995) *Genomics* 29(2):371-382); (approximately 28.3% identity over a 166 amino acid overlap) to the murine IL-9 receptor (SEQ ID NO:8; SP Accession Number Q01114; Renauld *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89(12):5690-5694) (see Figure 1A and 1B).

REMARKS

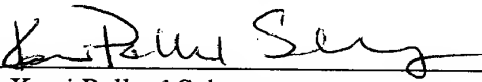
This Preliminary Amendment amends paragraphs of the specification to correctly reflect Figure identifications, specifically to refer to Figure 1 correctly as Figure 1A and 1B. Submitted concurrently herewith are Appendix A, Clean Copy of Amendments to Specification and Appendix B, Version to Show Changes Made to Specification.

Replacement pages 6, 7, 13, 14, and 33, are filed herewith with Response to Notice to File Corrected Application Papers solely to reflect the correct Figure identification. No new matter is entered by virtue of the amendments. Entry of the amendments made herein is respectfully requested.

December 4, 2001

Respectfully submitted,

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Appendix A**Clean Copy of Amendments to Specification**

At page 6, line 29 through page 7, line 5, please replace the paragraph with the following:

Figure 1A and 1B shows the amino acid sequence alignment for the human and murine 16445 proteins (SEQ ID NO:2 and SEQ ID NO:4, respectively) encoded by human 16445 (SEQ ID NO:1) and its murine orthologue 16445 (SEQ ID NO:3) with the human IL-2 receptor beta chain (hIL-2Rb; SP Accession Number P14784; SEQ ID NO:5), murine IL-2 receptor beta chain (mIL-2Rb; SP Accession Number P16297; SEQ ID NO:6), human IL-9 receptor (hIL-9R; SP Accession Number Q01113; SEQ ID NO:7), and murine IL-9 receptor (mIL-9R; SP Accession Number Q01114; SEQ ID NO:8). The sequence alignment was generated using the Clustal method.

At page 13, lines 12 through 17, please replace the paragraph with the following:

The h16445 protein displays similarity to the human IL-2 receptor beta chain (SEQ ID NO:5; approximately 36.9% identity over a 130 amino acid overlap), the murine IL-2 receptor beta chain (SEQ ID NO:6; 32.7% identity over a 110 amino acid overlap), the human IL-9 receptor (SEQ ID NO:7; approximately 29.7% identity over a 158 amino acid overlap), and the murine IL-9 receptor (SEQ ID NO:8; approximately 28.3% identity over a 166 amino acid overlap) (see Figure 1A and 1B).

At page 13, line 25 through page 14, line 2, please replace the paragraph with the following:

The murine clone, m16445, encodes an approximately 2.5 Kb mRNA transcript having the corresponding cDNA set forth in SEQ ID NO:3. This transcript has a 1587 nucleotide open reading frame (nucleotides 391-1976 of SEQ ID NO:3), which encodes a 529 amino acid protein (SEQ ID NO:4) having a molecular weight of approximately 58.3 kDa. An analysis of the full-length m16445 polypeptide predicts that the N-terminal 19 amino acids represent a signal peptide. This polypeptide represents the protein sequence encoded by the murine orthologue of the h16445 gene. The mouse 16445 protein shares approximately 64.4% identity with the human 16445 protein disclosed in SEQ ID NO:2 (see Figure 1A and 1B).

At page 77, lines 4-25, please replace the two paragraphs with the following paragraphs:

The identified clone h16445 encodes a transcript of approximately 2.3 Kb (corresponding cDNA set forth in SEQ ID NO:1). The open reading frame (nt 349-1965) of this transcript encodes a predicted 538 amino acid protein (SEQ ID NO:2) having a molecular weight of approximately 59.1 kDa. A search of the nucleotide and protein databases revealed that h16445 encodes a precursor polypeptide that shares similarity with several cytokine receptor proteins. An alignment of the protein sequences having highest similarity to the h16445 precursor polypeptide is shown in Figure 1A and 1B. The alignment was generated using the Clustal method with PAM250 residue weight table and sequence identities were determined by FASTA (Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444-2448).

The h16445 protein displays similarity to the human IL-2 receptor beta chain (approximately 36.9% over a 130 amino acid overlap; SEQ ID NO:5; SP Accession Number P14784; Hatakeyama *et al.* (1989) *Science* 244(4904):551-556). It also displays similarity to the murine IL-2 receptor beta chain (approximately 32.7% identity over a 110 amino acid overlap; SEQ ID NO:6; SP Accession Number P16297; Kono *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87(5):1806-1810); the human IL-9 receptor (approximately 29.7% identity over a 158 amino acid overlap; SEQ ID NO:7; SP Accession Number Q01113; Renauld *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89(12):5690-5694; Chang *et al.* (1994) *Blood* 83(11):3199-3205; Kermouni *et al.* (1995) *Genomics* 29(2):371-382); (approximately 28.3% identity over a 166 amino acid overlap) to the murine IL-9 receptor (SEQ ID NO:8; SP Accession Number Q01114; Renauld *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89(12):5690-5694) (see Figure 1A and 1B).

Appendix B

Version to Show Changes Made to Specification

At page 6, line 29 through page 7, line 5, please replace the paragraph with the following:

Figure 1A and 1B shows the amino acid sequence alignment for the human and murine 16445 proteins (SEQ ID NO:2 and SEQ ID NO:4, respectively) encoded by human 16445 (SEQ ID NO:1) and its murine orthologue 16445 (SEQ ID NO:3) with the human IL-2 receptor beta chain (hIL-2Rb; SP Accession Number P14784; SEQ ID NO:5), murine IL-2 receptor beta chain (mIL-2Rb; SP Accession Number P16297; SEQ ID NO:6), human IL-9 receptor (hIL-9R; SP Accession Number Q01113; SEQ ID NO:7), and murine IL-9 receptor (mIL-9R; SP Accession Number Q01114; SEQ ID NO:8). The sequence alignment was generated using the Clustal method.

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